In the Specification

Please enter the enclosed SEQUENCE LISTING into the specification.

Please amend the paragraph beginning at line 25 of page 10 as follows:

Figure 5. The partial amino acid sequence of ubiquitin-luciferase fusion proteins was evaluated in establishing the relative importance of the N-terminal residue in determining protein half-life (SEQ ID NOs: 82-88). Shadowed/boxed areas mark ubiquitin and luciferase sequences. Thick lines mark the position of deletions.

Please amend the paragraph beginning at line 23 of page 9 as follows:

In one embodiment, the N-terminal heterologous protein destabilization sequence is a cyclin destruction box or N-degron. In one embodiment the C-terminal heterologous protein destabilization sequence is a CL peptide, CL1, CL2, CL6, CL9, CL10, CL11, CL12, CL15, CL216, or CL17, SL17 (see Table 1 of Gilon et al., 1998, which is specifically incorporated by referenced herein), a C-ODC or a mutant C-ODC, e.g., a sequence such as HGFXXXMXXQXXGTLPMSCAQESGXXRHPAACASARINV (SEQ ID NO:81; corresponding to residues 423-461 of mODC), wherein one or more of the residues at positions marked with "X" are not the naturally occurring residue and wherein the substitution results in a decrease in the stability of a protein having that substituted sequence relative to a protein having the nonsubstituted sequence. For instance, a fusion polypeptide comprising a mutant C-ODC which has a non-conservative substitution at residues corresponding to residues 426, 427, 428, 430, 431, 433, 434, or 448 of ODC, e.g., from proline, aspartic acid or glutamic acid to alanine, can result in a fusion polypeptide with decreased stability, e.g., relative to a fusion polypeptide

with a non-substituted C-ODC.